au70a10.y MR4-NT014 MR3-NN021 MR4-NT014 HOA21-1-C DKFZp469B

BF948789 BF923639

BG898974 F CR767137 I AA336628 F BE766870 F BF923643 N

EST41242 RC2-NT011 MR4-NT014 MR4-NT014 MR4-NT014 PM1-NN120 QV2-TN017 MR4-NT014 PM1-NN120 GV2-TN017 MR4-NT014 MR4-NT014 MR7-NT014 S60374724 S60374724

BF963107

BF945175 BQ345410 BF923633

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

BF8875 (BI041998 NBI041248 NCD612964 BF961150 F

CR763018 I BF947155 N

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LEUYYU65
tigr-gss-dog-17000371093708 Dog Library Canis familiaris genomic,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                     Eukaryotan.

Eukaryotan Menazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutleria; Carnivora; Fissipedia; Canidae; Canis.

(bases 1 to 532)

Kirkness, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Kirkness, B.F., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .532
/organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_l: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                      The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                       BF923639
BC898974
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                             BF948789
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Canis familiaris
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Class: shotgun.
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BI032792 MR4-NN018
TOTAGA30 PMI-NN120
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AI745406 wc37d01.x
BI036662 MR4 NT014
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BF957658 PM1-NN120
                                                                 May 23, 2005, 23:05:16 ; Search time 1868 Seconds (without alignments) 427.917 Million cell updates/sec
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                                                                                                                                                                                                        68479088
       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                    34239544 segs, 19032134700 residues
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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99b_est2:

99b_est4::

90b_est6::

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90b_9881:
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BF957666 BF957653 BF957858

BI036862

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Contact: Simpson A.J.G.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                            Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 573)
1 (Bases I to 573)
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3 (Bascai Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
Fax: +55-11-2700492
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-NT0179-171100-004-h01&t53=2000-11-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 573.
                                                                                              BF921577 573 bp mRNA linear EST 19-JAN-2001 MR1-NT0179-171100-004-h01 NT0179 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/organism="Homo sapiens"
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Thunc Gene Index

Unpublished (1997)
Conteact: Robert Strausberg, Ph.D.
Conteact: Robert Strausberg, Ph.D.
Conteact: Robert Strausberg, Ph.D.
Famil: cgapbs-r@mail.nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordates, Catarrhini; Hominidae; Homo.

1 (bases 1 to 100)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
G., Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="NCI CGAP Ov39"
/note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT priming. Non-directionally cloned into the UDG sites of pAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research
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mRNA sequence.
      Euteleostomi;
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/lab_host="DH108"
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 83)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 2.4e+02;
5; Mismatches 0; Indels
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2745288"
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011200-009-b07&t3=2000-12-01&t4=1)
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/note="Organ: nervous tumor; Vector: puc18; Site_1: Smal;
/note="Organ: nervous tumor; Vector: Puc18; Site_1: Smal; Vector: Puc18; Vector:
                                                                                                                                                                      Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-NT0179-
071100-003-F02&t3=2000-11-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 100.
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(bases I to 10.5)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Magai, M.A., Gosta, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., Geoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Harre, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Fax: +55-11-2707001
Faxi +55-11-2707001
Final: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-
                                  Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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Best Local Similarity 73.7%; Pred. No. 2.4e+02;
Matches 14; Conservative 5; Mismatches 0; Indels
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Laboratory of Cancer Genetics
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BF958934.1 GI:12376209
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Homo sapiens
                                                                                                                                               Tel: +55-11-2704922
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1...102
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/dev_stage="mRNA"
/dlow_stage="mNN1200"
/clonellh="mNN1200"
/note="Organ: nervous normal; Vector: puc18; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-NN1011-100
300-110-g04&t3=2000-03-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence start: 11
Location/Qualifiers
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CM4-NN1011-100300-110-g04 NN1011 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 4; 1
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
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/organism="Homo sapiens"
Seg primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 101.
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/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                       Location/Qualifiers
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Mammalia; Eutheria;
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ORIGIN

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CD612965.1
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/clone lib="$20T665307"
/clone lib="$20T665307"
/clone lib="$20T665307"
/clone lib="$20T665307"
/site 2: Not1; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof* by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
/clone_lib="NN1011"
/note="Organ: nervous normal; Vector: puc18; Site_1: Smal, Site_2: Smal, A minl-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the pUC18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 124)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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K-EST0090952 S20T665307 Homo sapiens CDNA clone S20T665307-15-H01
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Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fel: +82-42-860-4409
Fax: +82-42-860-4409
                                                                                                                                                                                                                                     ch 90.5%; Score 19; DB 2; Length 119; I Similarity 73.7%; Pred. No. 2.5e+02; 14; Conservative 5; Mismatches 0; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-15-H01"
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Plate: 15 row: H column: 01
High quality sequence stop: 124.
Location/Qualifiers
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BM821731
BM821731.1 GI:19178144
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Homo sapiens
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Matches 14; Conserv
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1 (bases 1 to 136)

1 (kases 1 to 136)

1 (kases 1 to 137)

2 (kases 1 to 137)

2 (kases 1 to 137)

3 (kases 1 to 137)

4 (kases 1 to 137)

5 (kases 1 to 137)

6 (kases 1 to 137)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 137)
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Length 124;
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Pred. No. 2.6e+02;
5; Mismatches 0; Indels
                                               0; Indels
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56043322H1 FLP Homo sapiens cDNA, mRNA sequence.
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/note="Vector: pDrive Cloning Vector"
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
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Email: Gfu@incyte.com.
Location/Qualifiers
Score 19; DB 4; I
Pred. No. 2.5e+02;
5; Mismatches 0;
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/mol_type="mRNA"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Location/Qualifiers
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  90.5%;
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Similarity 73.7%;
14; Conservative
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Homo sapiens
    Query Match
Best Local Similarity 73.7
Matches 14; Conservative
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ORIGIN

BQ339862/c

RESULT 10

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DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

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D45267 142 bp mRNA linear EST 30-DEC-1995
HUMHG1194 Human cerebral cortex Homo sapiens cDNA, mRNA seguence.
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РМЛ-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.
BQ339466
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1 (basel to 1 Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Institute of Madical Science
Inversity of Tokyo
Shirokanedi 4-6-1, Minato-ku, Tokyo, Japan 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.5%; Score 19; DB 7; 73.7%; Pred. No. 2.6e+02;
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/organism="Homo
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Fax: 03-5449-5445
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 138)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Brunstein, A., Garvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ339862 11200-010-f07 NN1200 Homo sapiens cDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PMI&t2=PMI-NN1200-
011200-010-f07&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 35.
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudence 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                               Length 137;
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/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive_Cloning_Vector"
                                                                                                                                              DB 6; 2.6e+02;
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Pred. No.
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Best Local Similarity 73.7%;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0065"
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 148)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                          This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.hr/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-051100-004-hl2&t3=2000-l1-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 34.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                Email: asimpson@ludwig.org.br
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                                    Tel: +55-11-2704922
Fax: +55-11-2707001
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/mol_type="maxn" cref control of the property 
                                                                                                                                                                                                                                                      /note="Organ: lung_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
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Bscribano, J., Ortego, J. and Coca-Prados, M.
Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: Transcription and synthesis of plasma proteins J. Biochem. 118 (5), 921-931 (1995)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Department of Ophthalmology and Visual Science
Yale University Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: miguel coca-prados@quickmail.yale.edu Seq primer: 1\overline{3}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 Cedar Street, New Haven, CT 06520-8061
Tel: 2037852742
Fax: 2037856123
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2.6e+02;
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Pred. No. 2.6e+
5; Mismatches
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sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae, Homo.

1 (bases 1 to 169)

1 (barei, M. a. deoliveira, P. S., Bucher, P., Jongeneel, C. V., Soares, F. Brentani, R. S., Seise, S. S. Simpson, D. H., Sangson, A., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Singson, A. ...
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Fax: +55-11-2707010
Fig. +55-11-2707010
Fig. +57-11
Fig. +
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//mol_trop="mkNA"
/db_xref="taxon:9606"
/de_stage="Adult"
/clone_lib="Nroll0"
/note="Organ: nervous tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                    BE766895 169 bp mRNA linear EST 19-SEP-2000 RC2-NT0110-050600-013-£03 NT0110 Homo sapiens CDNA, mRNA sequence. BE766895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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/organism="Homo sapiens"
GCAGCAGAGUCUUCAUCAU 19
                                                  69 GCAGCAGAGTCTTCATCAT 51
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Homo sapiens (human)
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BE766895/c
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MEDLINE
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AUTHORS
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Gaps ö Query Match 90.5%; Score 19; DB 2; Length 169; Best Local Similarity 73.7%; Pred. No. 2.7e+02; Matches 14; Conservative 5; Mismatches 0; Indels

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Search completed: May 24, 2005, 00:21:54 Job time : 1874 secs

(UIYRU) NNAJA 39A9 SIHT

2, Appli 3, Appli 6149, Ap

Sequence Sequence Sequence

Sequence 2, Appli Sequence 3, Appli Sequence 6149 Sequence 21431, A Sequence 2971, Appli Sequence 2971, Appli

Sequence 8 Sequence 8 Sequence 8

Sequence:

Run on:

Searched:

Database

Result No.

Sequence Sequence

Sequence

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APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: With Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
90.5%; Score 19; DB 2; Length 181;
Best Local Similarity 73.7%; Pred. No. 21;
Matches 14; Conservative 5; Mismatches 0; Indels
       US-09-270-767-30143
US-09-313-294A-2815
US-09-313-294A-1242
US-09-172-711-3
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US-09-6107-532A-2971
US-09-107-532A-2971
US-09-107-532A-2971
US-09-107-532A-2971
US-09-614-124B-89
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US-09-614-124B-89
US-09-614-124B-89
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US-09-618-89-18-89
US-09-618-81-89
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300 South Wacker Drive, 32nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: No. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELEPHONE: 312-913-0001
TELEPAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08485657A
Patent No. 5942389
GENERAL INFORMATION:
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nucleic acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs
STRANDEDNESS: single
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CITY: Chicago
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12, Appl
17403, A
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1618, Ap
139518,
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3749, Ap
201815,
3, Appli
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333.610 Million cell updates/sec
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                                                                                               May 23, 2005, 23:07:41 ; Search time 103 Seconds
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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PCT-US55-02303-14
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US-09-513-999C-11015
US-09-713-550-15
US-09-912-50-15
US-09-912-915
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US-09-959-016-17403
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US-08-485-657A-14
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                                                                                                                                                                                                                                                                1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Patent No. 5942389
GENERAL INFORMATION:
APPLICANT: Gidschling, Deborah J
APPLICANT: Gidschling, Deborah J
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/485,657A FILING DATE: 07-JUN-1995 CLASSIFICATION: 800
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                                                                                                                                                                                                               90.5%; Score 19; DB 5; 73.7%; Pred. No. 21;
                                                                                                                                                                                                                                                          5; Mismatches
  PCT/US95/02303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: No. 594389nan, Kevin E
REGISTRATION UNDER: 35,303
REFERENCE/DOCKET NUMBER: 93,35
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCAGCAGAGUCUUCAUCAU 19
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                                                                                                                                                                                                                                                                                                                                        71 GCAGCAGAGTCTTCATCAT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
                                                            LENGTH: 181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                 Best Local Similarity 73.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 73.7
Matches 14; Conservative
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APPLICATION NUMBER: PC
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                               linear
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                                                                                                                          TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-485-657A-14/C
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                                                                                                                                                                                                                    Query Match
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                                                                                                Sequence 19, Application US/0936380
; Sequence 19, Application US/0936380
; Patent No. 6541603
; GENERAL INFORMATION:
    APPLICANT: Gudkov, Andrei
    APPLICANT: Gudkov, Andrei
    TITLE OF INVENTION: Genes and Genetic Elements Associated
    TITLE OF INVENTION: with Sensitivity to Cisplatin
    NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
    ADDRESSER MCDORNEIL Boehnen Hulbert & Berghoff
    STREET: 300 South Wacker Drive, 32nd Floor
    CITY: Chicago
    STATE: Illinois
    COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%; Score 19; DB 4; Length 181; 73.7%; Pred. No. 21;
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TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 6541603nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0002
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PCT-US95-02303-18/c
; Sequence 18, Application PC/TUS9502303
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,900
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    71 GCAGCAGAGTCTTCATCAT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.73
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: CDNA
US-09-366-380-19
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                                                                                         US-09-366-380-19/c
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US-09-513-999C-11015/c

US-09-513-999C-11015/c

Sequence 11015, Application US/09513999C

Patent No. 67836II

GENERAL INFORMATION:

APPLICANT: Duclart, A.

APPLICANT: Duclart, A.

TITLE OF INVENTION:

Patent No. 678396I

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT PILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER: OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 11015

LENGTH: 275
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Pred. No. 24;
                                                                                                                                                                                       DB 5; Length 195;
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US-09-640-173-15/c

Sequence 15, Application US/09640173

Sequence 15, Application US/09640173

Sequence 15, Application US/09640173

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 210121.484C2

CURRENT FILING DATE: 2000-08-15
                                                                                                                                                                                                                                               5; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                    Score 19;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GCAGCAGAGTCTTCATCAT 108
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                                                                                                                                                                                                                                                                                                                                                                  85 GCAGCAGAGTCTTCATCAT 67
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                                                                                                                                                                                 Query Match
Best Local Similarity 73.7%;
Matches 14; Conservative
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Best Local Similarity 73.7'
Matches 14; Conservative
                                  STRANDEDNESS: single TOPOLOGY: linear MLECULE TYPE: cDNA PCT-US95-02303-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-513-999C-11015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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LENGTH: 396
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         Sequence 14, Application US/09366380
Fatent No. 654603
Fatent No. 654603
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Gudkov, Andrei
FITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: With Sensitivity to Cisplatin
FITLE OF INVENTION: WITH SENSITIVE SENSITI
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: With Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 25
COMPUTER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,380
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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NAME: No. 6541603nan, Kevin E
REGISTRATION NUMBER: 35,303
REPERNCE/DOCKET NUMBER: 93,354-N
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PARIOR APPLICATION NUMBER: 08/199,900
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCAGCAGAGUCUUCAUCAU 19
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 73.7
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PCT-US95-02303-14/c
US-09-366-380-14/c
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JS-09-970-966-15/c
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; APPLICANT: Xiangohun
; APPLICANT: Algate, Paul A.; APPLICANT: Algate, Paul A.; APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: THERRAPY AND DIAGNOSIS OF OVARIAN CANCER; FILE REFERENCE: 210121.484C5; CURRENT FALLICATION NUMBER: US/09/825,294; CURRENT FILICATION TOWNER: 2001-04-03; NUMBER OF SEQ ID NOS: 215; SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                                                                                                                                                     APPLICANT: Xu, Jangchun
APPLICANT: Xu, Jangchun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C4
CURRENT APPLICATION NUMBER: US/09/713,550
CURRENT PILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 205
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 90.5%; Score 19; DB 4; Length 396; 1 Similarity 73.7%; Pred. No. 24; 14; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 396;
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Indels
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5; Mismatches
5; Mismatches
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                                                                                                                                              US-09-713-550-15/c

'Sequence 15, Application US/09713550

'Patent No. 6617109

'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature;
CCATION: (1)...(396)
US-09-713-550-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCAGCAGAGUCUUCAUCAU 19
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                                                         77 GCAGCAGAGTCTTCATCAT 59
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                                   1 GCAGCAGAGUCUUCAUCAU 19
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Matches 14; Conservative
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapien
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Matches 14; Conserv
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US-09-825-294-15/c
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LENGTH: 396
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 15
LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                            APPLICANT: STELLY.
APPLICANT: Molesh, David Alan
APPLICANT: Molesh, David Alan
APPLICANT: Molesh, David Alan
APPLICANT: Molesh, David Alan
APPLICANT: Mu, Jiang, Steven P.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COVARIAN CANCER
FILE REPERENCE: 210121.484C6
CURRENT APPLICATION UNDRER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.5%; Score 19; DB 4; Length 482; 73.7%; Pred. No. 24;
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Sequence 13267/C

Sequence 13267, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobcert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 0545 PR2
CURRENT APPLICATION HUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

SOFTWARE: Patent.pm

SEQ ID NO 13267

LENGTH: 482
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US-09-513-99C-3749/C
; Sequence 3749, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: DURAB Milne Edwards, J.B.
; APPLICANT: Duclert, A.
Sequence 15, Application US/09970966
Patent No. 6720146
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 333
CTHER INFORMATION: n = A,T,C or G
US-09-970-966-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 GCAGCAGAGTCTTCATCAT 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCAGCAGAGUCUUCAUCAU 19
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                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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Matches 14; Conserv
                                              GENERAL INFORMATION:
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US-09-949-016-201815

Sequence 201815, Application US/09949016

Sequence 201815, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITHER TOO 104-14

PRIOR APPLICATION NUMBER: 60/21,768

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 201815

LENGTH: 601
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APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
File REFERENCE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3749
LENGTH: 491
TYPE: DNA
CORGANISM: Homo sapiens
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 108..161
OTHER INFORMATION: SCORE 6.3
OTHER INFORMATION: SEQ LLFVGLLLTWESG/QV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 GCAGCAGAGTCTTCATCAT 108
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Best Local Similarity 73.7%;
Matches 14; Conservative 5
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 108..455
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; ORGANISM: Human
US-09-949-016-201815
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RESULT 15 US-09-659-791A-3/c

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OPPINE BARAINK (USPTO)

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May 23, 2005, 21:40:56; Search time 255 Seconds (without alignments) 487.508 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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21
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12:
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                                                                                                     Run on:
                                                                                                                                                                          Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|                               |          |          |          |          |          |                   |                    |                    |                    |                   |                   |                    |                    | •                  |                    |                    |                    |                    |                    |                    |
|-------------------------------|----------|----------|----------|----------|----------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| Description                   | RNAi     | RNAi     | RNAI     | RNAi     | RNAi     | Adl70445 RNAi for | Aaa94226 Human tes | Acf36398 TRPM-2 an | Adm83069 Human TRP | Adl70464 RNAi for | Adl70430 RNAi for | Adl70406 Antisense | Adl70521 Human clu | Aat00416 Genetic s | Aac06940 Human sec | Aaf94824 Human ova | Abl48774 Ovarian c | Abt03091 Human ova | Adm10684 Human ova | Adj11014 Represent |
| ID                            | ADL70465 | ADL70431 | ADL70522 | ADL70523 | ADL70444 | ADL70445          | AAA94226           | ACF36398           | ADM83069           | ADL70464          | ADL70430          | ADL70406           | ADL70521           | AAT00416           | AAC06940           | AAF94824           | ABL48774           | ABT03091           | ADM10684           | ADJ11014           |
| DB :                          | 12       | 12       | 12       | 12       | 12       | 12                | ო                  | 10                 | 11                 | 12                | 12                | 12                 | 12                 | N                  | m                  | 4                  | 9                  | 9                  | 11                 | 12                 |
| å<br>Query<br>Match Length DB | 21       | 21       | 19       | 19       | 19       | 19                | 21                 | 21                 | 21                 | 21                | 21                | 21                 | 23                 | 195                | 275                | 396                | 396                | 396                | 396                | 396                |
| &<br>Query<br>Match           | 100.0    | 100.0    | 90.2     | 90.5     | 90.5     | 90.5              | 90.5               | 90.5               | 90.5               | 90.5              | 90.5              | 90.5               | 90.5               | 90.5               | 90.8               | 90.5               | 90.5               | 90.5               | 90.5               | 90.5               |
| Score                         | 21       | 21       | 19       | 19       | 19       | 19                | 19                 | 19                 | 19                 | 19                | 19                | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 |
| Result<br>No.                 | -        | ~        | c<br>3   | 4        | υ<br>2   | φ                 | 7                  | œ                  | თ                  | c 10              | c 11              | 12                 | c 13               | c 14               | c 15               | c 16               | c 17               | c 18               | c 19               | c 50               |

| ω _                  | Human    |          |          | Aac03751 Human sec | Ach30243 Human tes | Ach43944 Human foe | Aav89150 EST clone | Aaz42136 Human nor | Abq56105 Human ova | Aaa43857 Human sec | Abz83527 Toxicolog | Acc90611 Human CGD | Human    |          | Acc90610 Human CGD | Acc90622 Human CGD | Adi02673 Human cDN | Aas44948 cDNA enco | Abs78654 Human cDN | Acc90609 Human CGD | _        | Aaq11503 Cytolysis | Abn99666 Human clu |
|----------------------|----------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|
| ADM43275<br>ACH44960 | ACH15312 | ACH44965 | ACH25299 | AAC03751           | ACH30243           | ACH43944           | AAV89150           | AAZ42136           | ABQ56105           | AAA43857           | ABZ83527           | ACC90611           | ACC90613 | ACC90621 | ACC90610           | ACC90622           | ADI02673           | AAS44948           | ABS78654           | ACC90609           | ABN99656 | AAQ11503           | ABN99666           |
| 12                   | ο (      | on .     | σ        | m                  | σ                  | σ                  | ď                  | ~                  | 9                  | m                  | 10                 | œ                  | œ        | œ        | œ                  | œ                  | 10                 | ហ                  | 9                  | 80                 | 9        | ~                  | 9                  |
| 396<br>461           | 462      | 465      | 490      | 491                | 491                | 492                | 512                | 572                | 704                | 922                | 1024               | 1067               | 1117     | 1315     | 1369               | 1373               | 1451               | 1568               | 1589               | 1610               | 1648     | 1651               | 1651               |
| 90.5                 | ω, i     | 'n       | ņ        | 'n                 | 'n                 | 'n                 | ĸ.                 | 'n.                | ĸ,                 | œ.                 | 'n.                | 'n.                | 'n       | 'n.      | 90.5               | 'n                 | s.                 | 90.5               | 90.5               | 90.5               | 90.5     | 'n                 | ı.                 |
| 9 6                  | 90       | 6        | 8        | 8                  | 8                  | 9                  | 90                 | 8                  | 8                  | 90                 | 90                 | 8                  | 8        | 8        | 8                  | 8                  | 9                  | 9                  | 90                 | 90                 | 90       | 8                  | 90                 |
| 19                   | 13       | 19       | 19       | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19       | 19       | 19                 | 19                 | 19                 | 19                 | 19                 | 19                 | 19       | 19                 | 19                 |
| 21                   | 23       | 24       | 25       | 26                 | 27                 | 28                 | 59                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35       | 36       | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43       | 44                 | 45                 |
| υυ                   | U        | U        | υ        | υ                  | ပ                  | U                  | υ                  | ပ                  | O                  | υ                  | υ                  | U                  | υ        | O        | υ                  | υ                  | U                  | υ                  | υ                  | υ                  | υ        | υ                  | U                  |
|                      |          |          |          |                    |                    |                    |                    |                    |                    |                    |                    |                    |          |          |                    |                    |                    |                    |                    |                    |          |                    |                    |

## ALIGNMENTS

ADL70465 standard; RNA; 21 BP.

RESULT 1 ADL70465 (first entry)

20-MAY-2004

ADL70465;

RNAi for human clusterin.

RNA interference, RNAi, short interfering RNA; siRNA; human, clusterin, cytostatic, neuroprotective, nootropic, gene silencing, DNA-RNA hybrid, Trougakos IP; Gleave ME, Signaevsky M, Beraldi E, /note= "OTHER= dTdT" Location/Qualifiers /\*tag= a /mod\_base= OTHER (UYBR-) UNIV BRITISH COLUMBIA. 21-AUG-2002; 2002US-0405193P. 03-SEP-2002; 2002US-0408152P. 20-MAY-2003; 2003US-0472387P. 21-AUG-2003; 2003WO-CA001277 WPI; 2004-226852/21. WO2004018676-A2 Key modified\_base Homo sapiens. 04-MAR-2004. Jansen B, Gonos ES; Synthetic. 

New RNA molecule less than 49 bases and having a sequence effective to mediate degradation or block translation of mRNA that is the transcriptional product of a target gene, useful for treating Alzheimer's

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Claim 20; SEQ ID NO 29; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-2002; 2002US-0405193P.
03-SEP-2002; 2002US-0408152P.
20-MAY-2003; 2003US-0472387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2003; 2003WO-CA001277
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL70522/c
ID ADL70522 standard; RNA; 19
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nes 21; Conservative
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                                                        The present sequence is the antisense strand of a short interfering RNA (siRNA) targeted to human clusterin. The sense strand is also provided ADL70464. The siRNA can be used to interfere with the expression of clusterin. also known as testosterone-repressed prostate message-2 (TRDM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate tumour cells following androgen withdrawal, and has also been shown to be critical for neuritic toxicity in mouse models of Alzheimer's disease. siRNAs of the invention can be used alone or in combination with other chemotherapy or apoptosis inducing treatments for the treatment of prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung melanoma, and also for the treatment of Alzheimer's disease.
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                               Claim 4; SEQ ID NO 10; 63pp; English.
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(GLEA/) GLEAVE M E.
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20-MAY-2003; 2003US-0472387P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL70431 standard; RNA; 21
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   disease or cancer
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The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligonocleotide ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin. The siRNAB molecules direct cleavage of clusterin mRNA. A method for regulating expression of bol-xi in a subject or cell line comprises administering an agent effective to modulate the amount of olusterin expression. In clusterin-expressing cells, expression of bol-xi is down-regulated when the effective amount of clusterin is reduced. Such inhibition is significant because bol-xi is known to act as an inhibitor
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Gonos ES;
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Claim 4; SEQ ID NO 68; 63pp; English.

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The present sequence is the sense strand of a short interfering RNA (sirRNA) targeted to a specific portion ADI70521 of human clusterin cDNA. The antisense strand is also provided ADI70521 of human clusterin cDNA. The antisense strand is also provided ADI70521 of human clusterin cDNA. Circlete with the expression of clusterin. Clusterin, also known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated as also been shown to be cumour cells following androgen withdrawal, and has also been shown to critical for neuritic toxicity in mouse models of Alzheimer's disease. SiRNAs of the invention can be used allone or in combination with other chemocherapy or apoptosis inducing treatments for the treatment of prostate cancer, bander cancer, lung cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and melanoma, and also for the treatment of Alzheimer's disease. In an example from the invention, the present anaplastic large cell lymphoma and melanoma, and also for the treatment of alzheimer's disease. In an example from the invention, the present anaplastic large cell in a example from the invention, the present anaplastic large cell in a cample from the invention, the present anaplastic large cell in a cample from the invention, the present and also for the treatment of all the present and all the present
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                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer cells. A reduction in clusterin transcript was observed.
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03-SEP-2002; 2002US-0408152P.
20-MAY-2003; 2003US-0472387P.
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Gonos ES;
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The present sequence is the antisense strand of a short interfering RNA (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA. The sense strand is also provided ADL70522. The siRNA can be used to interfere with the expression of clusterin. Clusterin, also known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated clumour cells following androgen in increased amounts by prostate tumour cells following androgen withdrawal, and has also been shown to be critical for neutric toxicity in mouse models of Alzheimer's disease. SIRNAs of the invention can be used alone or in combination with other commercer, aspectate cancer, sacromas such as osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer, or anglastic large cell lymphoma and melanoma, and also for the treatment of complastic large cell lymphoma and melanoma, and also for the bresent of Alzheimer's disease. In an example from the invention, the present sirNA was used to examine the effects of clusterin gene silencing in PC-3 prostate cancer cells. A reduction in clusterin transcript was observed.
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03-SEP-2002; 2002US-0408152P.
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                         The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligonuclectide ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL7045 mRNA. A method for regulating expression of bcl-xi in a subject or cell line comprises administering an agent effective to modulate the amount of ulusterin expression. In clusterin-expressing cells, expression of bcl-xi is down-regulated when the effective amount of clusterin is significant because bcl-xi is known to act as an inhibitor
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                                                                                                                                                     Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;
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         Claim 20; SEQ ID NO 42; 32pp; English.
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                                                                                                                                                                               Local Similarity
es 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    Key
modified_base
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(GLEA/) GLEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-2002;
02-DEC-2002;
                                                                                                                                                                                                                                                                                                                      20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapie
Synthetic.
                                                                                                                                                                                                                                                                                                   ADL70445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jansen B;
                                                                                                                                                                                                                                 13
                                                                                                                                                                        Query Match
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                        ADL70445
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The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL7043. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin. The siRNAs molecules direct cleavage of clusterin mRNA. A method for regulating expression of bcl.-xL in a subject or cell line comprises administering an agent effective to modulate the amount of clusterin expression. In clusterin-expressing cells, expression of bcl-xL is down-regulated when the effective amount of clusterin is reduced. Such inhibition is significant because bcl-xL is known to act as an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human testosterone-repressed prostate message-2 (TRPM-2, also known as clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to promote the regression of tumours, and oligonucleotides directed at human TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2 gene. These include prostate cancer, renal cell cancer and some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, testosterone-repressed prostate message-2; TRPM-2; clusterin; sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating prostatic tumors and renal cancers by antisense inhibition the testosterone-repressed prostate messenger-2 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human testosterone-repressed prostate message-2 antisense oligo #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 12; Length 19;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gleave M, Rennie PS, Miyake H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA94226 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
"...hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 73.7
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                       of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-2000
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BP.

(first entry)

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Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity, radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer; lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gleave M, Rennie PS, Miyake H, Nelson C,
                                                                                    Human TRPM-2 antisense oligonucleotide #4.
                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-2001; 2001US-00967726.
                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000WO-US004875.
28-SEP-2000; 2000US-0236301P.
10-AUG-2001; 2001US-00913325.
ADM83069 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLEA,) GLEAVE M.
(RENN,) RENNIE P S.
(MIYA,) MIYAKE H.
(MELS,) NELSON C.
(ZELL/) ZELLMEGER T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-778017/73.
                                                                                                                                                                                                                                                                                                                         US2003158130-A1
                                                                                                                                                             antisense; ss.
                                                                                                                                                                                                                                  Key
modified_base
                                                                                                                                                                                        Homo sapiens.
Synthetic.
                                                        03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                   21-AUG-2003.
                             ADM83069;
The invention relates to a compound consisting of an oligonuclectide with a phosphorothicate backbone throughout, in which: (a) sugars on nuclectide residues 1-4 and 18-21 are 2'-0-methoxyethyl modified, and the remaining nuclectides 5-17 are 2'-deoxy; and (b) the cytosines at remaining nuclectides 5-17 are 2'-deoxy; and (b) the cytosines at positions 1, 4 and 19 are 5-methylated Oligonuclectide shown in sequence ACF36398 (I) is used: (a) to delay progression of androgen-sensitive prostatic cancer cells to the androgen-independent state, in vivo or in vitro; (b) to treat prostatic cancer (after initially withdrawing candrogens to induce apptosis; and (c) to increase sensitivity of cancer cells (prostatic, renal, non-small cell lung, urothelial transitional, cells (prostatic, renal, non-small cell lung, urothelial transitional, increase stability in vivo and activity (both in vivo or in vitro) and result in a synergistic increase in effect when (I) is used with result in a synergistic increase in effect when (I) is used with chemical capanies or chemical properties and present sequence represents a specific example of an anti-apoptotic protein TRPM-2 (testosterone-
                                                                                                                                                                                                                                TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen; prostate cancer; anti-apoptotic protein; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostatic cancer, inhibits the testosterone-repressed prostate message-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified antisense oligonucleotide, useful particularly for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
90.5%; Score 19; DB 10; Length 21;
Best Local Similarity 73.7%; Pred. No. 34;
Matches 14; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repressed prostate message-2) antisense oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nelson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miyake H,
                                                                                                                                                                                                     TRPM-2 antisense oligonucleotide
            GCAGCAGAGUCUUCAUCAU 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 25; 44pp; English.
                           3 GCAGCAGAGTCTTCATCAT 21
                                                                                                               ACF36398 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2002; 2002US-00080794.
                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2003; 2003WO-US005305
                                                                                                                                                                        18-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                      WO2003072591-A1.
                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                    04-SEP-2003
                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                            ACF36398;
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/note= "Phosphorothioate backbone"

/mod\_base= OTHER

/\*tag= a

Location/Qualifiers

Zellweger T;

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                                                                                                                                                                 The present invention provides a method for treating cancer in which cancer cells express testosterone-repressed prostate message-2 (TRPM-2). The invention is useful for enhancing the chemo-sensitivity or radiationsensitivity of cancer cells for treating cancer such as prostate cancer, bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma (ECC). The invention is also useful in antisense gene therapy. The present sequence is human testosterone-repressed prostate message-2 (TRPM-2) antisense oligodeoxyribonucleotide (ODN).
Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells that expresses testosterone-repressed prostate message-2 (TRPM-2) comprises administering a composition that inhibits expression of TRPM-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.5%; Score 19; DB 11; Length 21; 73.7%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                    Claim 4; SEQ ID NO 4; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL70464 standard; RNA; 21 BP
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Best Local Similarity 73.79
Matches 14; Conservative
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ADL70464/C
ID ADL70
XX
AC ADL70
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Gaps

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1 GCAGCAGAGUCUUCAUCAU 19 

ઠે 엄 RESULT 9 ADM83069 RESULT

Synthetic

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Treating melanoma in a mammalian subject comprises administering to the subject a therapeutic agent effective to reduce the effective amount of clusterin in the melanoma cells.
                                                                RNAi; melanoma; cytostatic; gene silencing;
RNA; siRNA; DNA-RNA hybrid; ss.
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                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "OTHER= TT"
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(GLEA/) GLEAVE M E.
                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0408152P.
2002US-0319748P.
                                                                                                                                                                                                                                                                                                                                                                21-AUG-2003; 2003WO-CA001276
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20-MAY-2004 (first entry)
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Best Local Similarity 73.7
Matches 14; Conservative
                                    RNAi for human clusterin.
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/*tag=
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                                                                      Human; clusterin;
short interfering
                                                                                                                                                                                                                                                                                            WO2004018675-A1
                                                                                                                                                                                   Key
modified base
                                                                                                                             sapiens
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03-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                04-MAR-2004
                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jansen
                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the sense strand of a short interfering RNA (siRNA) targeted to human clusterin. The antisense strand is also provided ADL70465. The siRNA can be used to interfere with the expression of clusterin. Clusterin, also known as testosterone-repressed prostate message-2 (TRPA-2) or sulfated glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate tumour cells following androgen withdrawal, and has also been shown to be critical for neuritic toxicity in mouse models of Alzheimer's disease. SiRNAs of the invention can be used alone or in combination with other chemotherapy or apoptosis inducing treatments for the treatment of prostate cancer, sarcomas such as sosteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and melanoma, and also for the treatment of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New RNA molecule less than 49 bases and having a sequence effective to mediate degradation or block translation of mRNA that is the transcriptional product of a target gene, useful for treating Alzheimer's
                                                                                         RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin; cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beraldi E, Trougakos IP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 90.5%; Score 19; DB 12; Length 21; Local Similarity 73.7%; Pred. No. 34; Pred. No. 14; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signaevsky M,
                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "OTHER= dIdT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 9; 63pp; English.
                                                                                                                                                                                                                           Location/Qualifiers
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03-SEP-2002; 2002US-0408152P.
20-MAX-2003; 2003US-0472387P.
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                      (first entry)
                                                         RNAi for human clusterin
                                                                                                                                                                                                                                            0. .21
*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gleave ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-226852/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease or cancer.
                                                                                                                                                                                                                                                                                                                                      WO2004018676-A2
                                                                                                                                                                                                                                          nodified base
                                                                                                                                                                     sapiens
                        20-MAY-2004
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Jansen B, Gonos ES;

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The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin. The siRNAs molecules direct cleavage of clusterin mRNA. A method for regulating expression of bcl-xL in a subject or cell inte comprises administering an agent effective to modulate the amount of clusterin expression. In clusterin-expressing cells, expression of bcl-xL is down-regulated when the effective amount of clusterin is reduced. Such inhibition is significant because bcl-xL is known to act as an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.5%; Score 19; DB 12; Length 21; 73.7%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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ID ADL/
XX
AC ADL/
XX
DT 20-P
XX
DE ANL
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19

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Query Match Best Loc Matches ADL70430;

RESULT 11 ADL70430/c ID ADL70

Query Match

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Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
                                                                                                                           (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                               02-DEC-2002; 2002US-0319748P. 20-MAY-2003; 2003US-0472387P.
                                                                                                21-AUG-2003; 2003WO-CA001276
                                                                                                                                                WPI; 2004-226851/21.
                                                                                                                                GLEA/) GLEAVE M E.
                                                                               WO2004018675-A1
                        Key
modified_base
                                                           modified base
                                            modified base
            Homo sapiens
                                                                                                       21-AUG-2002;
03-SEP-2002;
                                                                                        04-MAR-2004
                 Synthetic.
                                                                                                                                        Jansen B;
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2002US-0405193P.

'\*tag= a
/mod\_base= OTHER
/note= "OTHER= 2'O-methoxyethyl modifications"

mod\_base= OTHER 'note= "OTHER= phosphorothioate nucleotides"

location/Qualifiers

Ω \*tag= /\*tag= c /mod\_base= OTHER /note= "OTHER= 2'O-methoxyethyl modifications"

/\*tag=

the present sequence is that of an antisense of sugginarized and content of the present sequence is that of the invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligomicleotide ADL704-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL7045 targeted to clusterin. The antisense oligomicleotides are complementary to a region of the clusterin mRNA spanning either the translation initiation site or the termination site. They may be modifications in the strain of state or the cernination site. They may be modifications in the stand may have 2' o-(2-methoxyethy1) (MOE) modifications in the s' and may have 2' o-(2-methoxyethy1) (MOE) modifications in the s' and 3' 'wings'. The present antisense oligomicleotide is particularly preferred. It is targeted to the translation initiation codon and next 6 codons of the targeted to the translation initiation codon and next 6 codons of the targeted to the translation initiation codon and next 6 codons of the cample from the invention, this antisense oligomicleotide provided a dose-dependent down-regulation of clusterin human melanoma cell line (607B) this alone was sufficient to lead to complete cell death. In one melanoma cell line (607B) this alone was sufficient to lead to complete cell death. In canothod method for regulating expression of bcl-xL in a subject or cell line comprises conditions in an author of the annial control of the annial cell of an intersine effective to modulate the amount of clustering and agent effective to modulate the amount of clustering and cells. expression. In clusterin-expressing cells, expression of bcl-xL is down-regulated when the effective amount of clusterin is reduced. Such inhibition is significant because bcl-xL is known to act as an inhibitor The present sequence is that of an antisense oligonucleotide targeted to Treating melanoma in a mammalian subject comprises administering to the subject a therapeutic agent effective to reduce the effective amount of clusterin in the melanoma cells. Claim 7; SEQ ID NO 4; 32pp; English.

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Seguence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
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ADI-70523. It was used in an example from the invention to demonstrate clusterin, gene silencing in PC-3 prostate cancer cells. Clusterin, also known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate cumour cells following androgen withdrawal, and has also been shown to be critical for neuritic toxicity in mouse models of Alzheimer's disease. siRNAs of the invention can be used alone or in combination with other chemotherapy or apoptosis inducing treatments for the treatment of prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer, anaplastic large call lymphoma and melanoma, and also for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New RNA molecule less than 49 bases and having a sequence effective to mediate degradation or block translation of mRNA that is the transcriptional product of a target gene, useful for treating Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin; cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
                                                                   Gaps
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DB 12; Length 21;
34;
                                                                Indels
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                                                                5; Mismatches
90.5%; Score 19; 73.7%; Pred. No. 3
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                                                                                                                                 1 GCAGCAGAGUCUUCAUCAU 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human clusterin target for RNAi
                                                                                                                                                                   3 GCAGCAGAGTCTTCATCAT 21
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03-SEP-2002; 2002US-0408152P.
20-MAY-2003; 2003US-0472387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-2003; 2003WO-CA001277.
                                                                                                                                                                                                                                                                                                                                                              ADL70521 standard; cDNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity
Matches 14; Conserv
                       Best Local Similarity
Matches 14; Conserv
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Gonos ES;
                                                                                                                                                                                                                                                                                                                                                                                                                           ADL/10521;
                                                                                                                                                                                                                                                                                             RESULT 13
ADL70521/c
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Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Human secreted protein 5' EST, SEQ ID NO: 11015.

(first entry)

06-OCT-2000

AAC06940;

BP.

AAC06940 standard; cDNA; 275

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The sequences represented by AAT00405-T00418 are genetic suppressor elements (GSEs). This sequence represents GSE HLG.10. This sequence shows be monology to the cDNA encoding testosterone-repressed prostatic message-2 (TRPM-2). These sequences were obtained from a CDNA library derived from the total CDNA of a cisplatin sensitive cell. Genetic suppressor elements confer resistance to platinum-based drugs (PDs), such as cisplatin. These functional GSEs can then be used to create probes for the parent gene. The probes can then be used in a method of measuring the level of GSE gene expression. The GSEs can be used in methods of diagnosis of cells are also used in methods to overcome resistance to PDs by measuring the level of expression of GSE genes. The GSEs are also used in methods to overcome resistance to PDs in cancer cells. The GSEs (or fragments of them) can be used to inhibit the GSEs (or fragments of them) can be used to inhibit the chemotherapy, a GSE can be transferred (either alone or with another gene) on an expression vector into blood progenitor cells from a cancer patient. The cells are returned to the patients circulation and allowed (using higher cisplatin concentrations than normal), this will thereby avoid toxic side effects to the immune system as the blood cells will be
                                                                                                                                                                                                                                                         Genetic suppressor element; GSE; platinum-based drug; cisplatin; chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic suppressor elements which confer resistance to platinum-based drugs, eg. cisplatin, on cancer cells - useful for enhancement of chemotherapy, and for diagnosis of resistance to these drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kirschling DJ, Gudkov A, Roninson IB;
                                                                                                                                                                                                                   Genetic suppressor element HL7.1.
                                                                                               AAT00416 standard; cDNA; 195 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Fig 17; 75pp; English
  21 GCAGCAGAGTCTTCATCAT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00199900.
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                                                                                                                                                                              (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-302718/39.
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                                                                                                                                                                                                                                                                                                                                                                               WO9522612-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-1995;
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                                                                                                                                                                              26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-1995.
                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                    AAT00416;
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                                                            RESULT 14
                                                                              AAT00416,
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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

Duclert A, Giordano J;

Dumas Milne Edwards J, WPI; 2000-500381/45.

(GEST ) GENSET

21-FEB-2000; 2000EP-00200610.

EP1033401-A2.

36-SEP-2000.

Homo sapiens

99US-0122487P.

26-FEB-1999;

Claim 1; SEQ ID NO 11015; 71pp + Sequence Listing; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local Similarity 73.73
Matches 14; Conservative
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1 GCAGCAGAGUCUUCAUCAU 19

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85

RESULT 15 AAC06940/c

Sequence EST and e Sequence

Sequence Sequence

nucleic

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Run on:

Sequence:

Searched:

Database

Result

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AX202086 Sequence
BC010514 Homo sapi
AX600209 Sequence
BX648414 Homo sapi
BV177186 sqnm93292
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                                                                                                   BD027496 Sequence
BD071299 Secreted
AK003199 Homo sapi
AK600212 Sequence
CQ716220 Sequence
BC019588 Homo sapi
AR20874 Sequence
M64722 Human TRPM-
A21577 blood plasm
AR20874 Sequence
M2515 Human compl
CQ786612 Sequence
AX774943 Sequence
XX74743 Human SP-40
                                          AX982464 S
BD117323 B
AX887886 S
BD027496 S
BD071299 AK093399 B
AR489627 8
AR493868 8
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Patent: WO 2004018676.A 10 04-MAR-2004;
The University of British Columbia (CA)
Location/Qualifiers
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/organism="synthetic construct"
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/db zref="texcn:32630"
/noTe="RNA1 for human clusterin"
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Sequence 10 from Patent W02004018676.
CQ786122 GI:45721225
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Sequence 29 from Patent WO2004018675.
CQ786640. GI:45721660
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Best Local Similarity 76.2%; Pred. No. 33;
Matches 16; Conservative 5; Mismatches
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 AR489627
AR493868
AR421770
AR421770
AR982464
BD117323
AX887886
BD071299
AK003399
AK00312
QC16220
BCC19588
AR208704
ARZO87704
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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PAT 24-MAR-2004

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                        Jansen, B.
Treatment of melanoma by reduction in clusterin levels
Patent: WO 2004018675-A 29 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
Location/Qualifiers
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Patent: WO 2004018676-A 67 04-MAR-2004;
The University of British Columbia (CA)
Location/Qualifiers
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/organism="synthetic construct"
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/noTe="RNAi for human clusterin"
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_kref="taxon:32630"
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Treatment of melanoma by reduction in clusterin levels
Parent: WO 2004018675-A 43 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin
Location/Qualifiers
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/organism="gynthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"
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/organism="synthetic construct"
/or_type="unassigned RNA"
/db xref="taxon:32630"
/noTe="RNAi for human clusterin"
                                                              /note="RNAi for human clusterin"
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                                                                                                                       Query Match
90.5%; Score 19; DB 6; 1
Best Local Similarity 73.7%; Pred. No. 3.1e+02;
Matches 14; Conservative 5; Mismatches 0;
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/db_xref="taxon:32630"
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CQ786653
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synthetic construct
other sequences, artificial sequences.
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synthetic construct
other sequences, artificial sequences.
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Jansen, B., Gleave, M.E., Signaevsky, M., Beraldi, E., Trougakos, I. and
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                    PAT 24-MAR-2004
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.1e+02;
5; Mismatches 0; Indels
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Patent: WO 2004018676-A 66 04-MAR-2004;
The University of British Columbia (CA)
Location/Qualifiers
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| mol type="unassigned DNA"
| db xref="taxon:32650"
| note="RNAi for human clusterin"
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                   CQ786639 21 bp DNA Sequence 28 from Patent WO2004018675. CQ786639
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Sequence 66 from Patent WO2004018676.
CQ786178
                                                                                                                             synthetic construct
other sequences; artificial sequences.

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 73.7%;
Matches 14; Conservative
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                                                                                                            synthetic construct
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 2004018676-A 9 04-MAR-2004;
The University of British Columbia (CA)
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/mol_type="unassigned DNA"
/mol_tref="taxon:32630"
/note="RNA! for human clusterin"
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synthetic construct
other sequences; artificial sequences.
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CQ786615.
CQ786615.1 GI:45721635
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Sequence 9 from Patent WO2004018676.
 Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                  GCAGCAGAGUCUUCAUCAU 19
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CQ786121.1 GI:45721224
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Homo sapiens
14; Conservative
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Matches 14; Conservative
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Query Match

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RESULT

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unclassified.
E 1 (bases 1 to 195)
KS Kirschling,D.J., Gudkov,A. and Roninson,I.B.
Genes and genetic elements associated with sensitivity to platinum-based drugs
platinum-based drugs
Location/Qualifiers
Location/Qualifiers
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             1 (bases 1 to 181)
Kirschling, D.J., Gudkov, A. and Roninson, I.B.
Genes and genetic elements associated with sensitivity to
platinum-based drugs
Patent: US 6541603-A 19 01-APR-2003;
Location/Qualifiers
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 37963 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                       Length 181;
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Best Local Similarity 73.7%; Pred. No. 2.8e+02;
Matches 14; Conservative 5; Mismatches 0; Indels
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Sequence 37963 from Patent W002070737.
CQ693037
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Unclassified.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                            Liew, C.C., Marshall, W.E. and Zhang, H. Compositions and methods relating to osteoarthritis Patent: WO 02070737-A 33018 12-SEP-2002; Chondrogene Inc. (CA)
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Pred. No. 2.7e+02;
5; Mismatches 0; Indels
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             Length 255;
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73.7%; Pred. No. 2.7e+02;
tive 5; Mismatches 0; Indels
                                              0; Indels
                                                                                                                                                                                         linear
           Score 19; DB 6; 1
Pred. No. 2.7e+02;
5; Mismatches 0;
                                                                                                                                                                               Sequence 33018 from Patent W002070737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
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/mol_type="unassigned DNA"
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Matches 14; Conservative 5
                90.5%;
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Homo sapiens
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Best 14, Conservative
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CQ688092/c
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VERSION
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TITLE
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AUTHORS
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JOURNAL
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Search completed: May 23, 2005, 23:50:37 Job time: 1718 secs

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May 23, 2005, 23:16:37 ; Search time 341 Seconds (without alignments) 377.650 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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21
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|    | Description              | 1 |                      | Sequence 10, Appl | Sequence 42, Appl | Sequence 43, Appl | Sequence 67, Appl | Sequence 68, Appl | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 28, Appl |
|----|--------------------------|---|----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
|    | ΩI                       |   | 17 US-10-646-391A-29 | US-10-646-436-10  | US-10-646-391A-42 | US-10-646-391A-43 | US-10-646-436-67  | US-10-646-436-68  | US-09-944-326-4   | US-09-967-726A-4  | US-10-080-794-4   | US-10-646-391A-4  | US-10-646-391A-28 |
|    | DB                       |   | 17                   | 17                | 17                | 17                | 17                | 17                | σ                 | 10                | 16                | 17                | 17                |
|    | Query<br>Match Length DB |   | 21                   | 21                | 19                | 19                | 19                | 19                | 21                | 21                |                   | 21                | 21                |
| 40 | Query                    |   | 100.0                | 100.0             | 90.5              | 90.5              | 90.5              | 90.5              | 90.5              | 90.5              | 90.5              | 90.5              | 90.5              |
|    | Score                    |   | 21                   | 21                | 19                | 19                | 19                | 19                | 19                | 19                | 19                | 19                | 19                |
|    | ult.<br>No.              |   | ٦                    | 7                 | М                 | 4                 | S                 | 9                 | 7                 | œ                 | σ                 | 10                | 11                |
|    | Result<br>No.            |   |                      |                   | υ                 |                   | υ                 |                   |                   |                   |                   |                   | Ų                 |
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| U          | 12                              | 13                 | 90.5          | 21                        | 11   | US-10-646-436-9  |                       |  |
|------------|---------------------------------|--------------------|---------------|---------------------------|------|--|-----------------------|--|
|            | 13                              | 19                 | 0 0           | 5 5                       | 18   | US-10-828-394-5  |                       |  |
| (          | # U                             | א פ                | <b>&gt;</b> < | 7 6                       | 1 0  | US-10-828-343-5  | Sequence 5, Appli     |  |
| v          | 16                              | 19                 | 0             | းထ                        | 17   | US-10-404-579-19   | Sequence 19, Appl     |  |
| U          | 17                              | 19                 | 0             | o                         | 17   | US-10-404-579-14   | Sequence 14, Appl     |  |
| U          | 18                              | 19                 | 0             | S.                        | 17   | US-10-242-535A-37963   | Sequence 37963, A     |  |
| U          | 19                              | 13                 | 0             | ഗി                        | 17   | US-10-085-783A-37963   | Sequence 37963, A     |  |
| U (        | 2.0                             | J -                | 0 0           | - 1                       | 17   | US-10-242-535A-33018   | Sequence 33018, A     |  |
| י כ        | 22                              | 7 -                | <b>&gt;</b> < | - c                       | 1 1  | US-10-083-783A-33018   | Seguence 33018, A     |  |
| ט          | 23                              | 161                | 90.5          | 306                       | 11   | 17 US-10-242-333A-28941  | Sequence 28941, A     |  |
| υ          | 24                              | 19                 | 0             | 4                         | 13   | US-10-696-639-2963   |                       |  |
| υ          | 25                              | 19                 | 0             | σ                         | 6    | US-09-825-294-15   | equence               |  |
| υ          | 26                              | 19                 | 0             | 9                         | 6    | US-09-970-966-15   |                       |  |
| ပ          | 27                              | 19                 | 0             | σ                         | 12   | US-10-212-677-15   | Sequence 15, Appl     |  |
| U          | 28                              | 13                 | 0             | g)                        | 11   | US-10-361-811-15   | Sequence 15, Appl     |  |
| υ          | 29                              | 13                 | 0             | σ,                        | 17   | US-10-369-186-15   | Sequence 15, Appl     |  |
| υ          | 30                              | 61                 | 0 (           | o١                        | 2:   | US-09-918-995-32172  | Sequence 32172, A     |  |
| U I        | 3.I                             | 61.                | 9             | ο١                        | 9 ;  | US-09-918-995-2524   | Sequence 2524, Ap     |  |
| U (        | 2.5                             | 7 .                | 0             | o                         | 2 6  | US-09-918-995-32177  | Sequence 32177, A     |  |
| י כ        | n <                             | n c                | 0             | n σ                       | 9 6  | 115 00 010 00 11411  | sequence 12311, A     |  |
| ט נ        | # L                             | א כ                | э с           | n c                       | 2 5  | US-US-SIB-SS-I/455   | Sequence 1/455, A     |  |
| ט כ        | ה ע                             | n 0                | 2             | 707                       | 2 5  | US-US-918-993-31136<br>IR-10-264-049-1985  | Sequence Silso, A     |  |
| י נ        | 37                              | 1 0                | ٥ د           | פי פ                      | 10   | US-10-264-043-1363   | Sequence 1909, Ap     |  |
| , (        |                                 | 2 0                | <b>o</b> c    | 3 -                       | 1 6  | 115-10-401-213-91  | Sequence 31, Appl     |  |
| י נ        | 0 0                             | 7 6                | ) C           | 15                        | 1 0  | 110-10-491-213-93  | Sequence 33, Appr     |  |
| , (        | J 4                             | ם ב                | ) C           | 7 7                       | 1 5  | 118-10-491-213-101   | ט ס                   |  |
| י כ        | 5 -                             | , o                | ) c           | 2 0                       | 1 -  | 116-10-491-213-90  | edrence               |  |
| י כ        | T C V                           | h 0                | 2 0           | 7 4                       | אַ ר | US-10-491-213-102  | ednence               |  |
| י כ        | 7.5                             | h 0                | 0             | ת<br>דים                  | 3 6  | US-IO-ISS-UIS-ZI4  | ednence               |  |
| ט כ        | 4.5                             | γ <del>-</del>     | 20            | 1568                      | 11   | US-10-291-1/2-29<br>118-10-221-278-29  | Seguence 29, Appl     |  |
| י נ        | * "                             | 7 -                | 50            | מים                       | 7 6  | US-10-401-278-29   | eduence               |  |
| ر          | n<br>r                          | C<br>T             | •             | 7                         | 13   | 68-517-161-01-60   | מלחבווכם              |  |
|            |                                 |                    |               |                           | •    | ALIGNMENTS   |                       |  |
|            |                                 |                    |               |                           |      |  |                       |  |
| RESU       | RESULT 1                        | 010-010            |               |                           |      |  |                       |  |
| Se         | quence                          | 29. Ap             | plicat        | tion US                   | /106 | 46391A   |                       |  |
| 2          | Publication No. US20040082534A1 | on No.             | US20(         | 0400825                   | 34A1 |  |                       |  |
| В          | GENERAL INFORMATION             | NFORMA             | TION:         |                           |      |  |                       |  |
| α,<br>     | APPLICANT: Gleave,              | I: Gle             |               | Martin                    | ,    |  |                       |  |
| ⊄ E        | PPLICAN                         | בייהיד             | nsen,         | Burkna                    |      | Man Daniel Comment of the Comment of | [410]                 |  |
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| , c        | CURRENT FILING DATE             | DITTING            | DATE:         | . 2003-08                 | 2 6  | 160'   |                       |  |
|            | RIOR AP                         | PLICAT             | NOT           | TWARR                     | 2 2  | 0/405.193  |                       |  |
|            | PRIOR FIL                       | LING               | ATE           | R FILING DATE: 2002-08-21 | 2.5  |  |                       |  |
|            | RIOR AP                         | PLICAT             | TON MI        | IMBER: 1                  | 18.  | 0/319.748  |                       |  |
| Δ.         | RIOR FII                        | LING               | ATE:          | 2002-12                   | -02  |  |                       |  |
| Δ,         | RIOR API                        | PLICAT             | TON ML        | JMBER: 1                  | JS 6 | 60/408,152   |                       |  |
| Δ,         | RIOR FIL                        | LING D             | ATE: 2        | 2002-09.                  | 9-03 |  |                       |  |
| а.         | PRIOR API                       | APPLICATION NUMBER | TON M         | ••                        |      | 60/473,387   |                       |  |
| <u>п</u> , | RIOR FI                         | LING D             | ATE:          | 35                        | -20  |  |                       |  |
| z (        | NUMBER OF                       | SE                 | ID NOS        | O ID NOS: 43              |      |  |                       |  |
| ν <u>Θ</u> | SOFTWARE                        | : Pate             | nc in         | /erвıoп                   | 3.   |  |                       |  |
| a<br>      | LENGTH.                         | ν <del>-</del>     |               |                           |      |  |                       |  |
|            | TYPE: DNA                       | 4                  |               |                           |      |  |                       |  |

Query Match
100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0;

; OTHER INFORMATION: RNAi for human clusterin US-10-646-391A-29

TYPE: DNA ORGANISM: artificial

FEATURE:

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Gaps

1 GCAGCAGAGUCUUCAUCAUTT 21

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1 GCAGCAGAGUCUUCAUCAU 19
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100.0%;
Query Match
Best Local Similarity 73.7%;
Matches 14; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gleave, Martin
APPLICANT: Jansen, Burkh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: artificial
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Publication No. US20040082534A1

Sequence 42, Application US/10646391A

Publication No. US20040082534A1

SEQUENCE AND CONTROL OF TEACHER OF TITLE OF INVERMITION: TEACHER OF TITLE OF INVERTION: TEACHER OF TITLE OF INVERTION: TEACHER OF TILING DATE: 2003-08-21

PRIOR APPLICATION NUMBER: US 60/406,193

PRIOR FILING DATE: 2002-08-21

PRIOR FILING DATE: 2002-02-12

PRIOR FILING DATE: 2002-12-02

PRIOR FILING DATE: 2002-12-02

PRIOR PRIOR PRIOR NUMBER: US 60/408,152

PRIOR APPLICATION NUMBER: US 60/473,387

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/473,387

PRIOR APPLICATION NUMBER: US 60/473,387
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                                                                                                                                      US-10-646-436-10

| Sequence 10, Application US/10646436 |
| Sequence 10, Application US/10646436 |
| Sequence 10, Application No. US2004009688241 |
| GENERAL INPORMATION: |
| APPLICANT: Jansen, Burkhard |
| APPLICANT: Gleave, Martin |
| APPLICANT: Signaevsky, Maxim |
| APPLICANT: Becaldi, Eliana |
| APPLICANT: Gleave, Namin |
| APPLICANT: Gleave, Namin |
| APPLICANT: Gleave, Maxim |
| APPLICANT: Gleave, Namin |
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| APPLICANT: Gleave, Maxim |
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| FILE REFERENCE: US-030-08-21 |
| PRIOR FILING DATE: 2002-09-03 |
| PRIOR FILING DATE: 2003-09-03 |
| PRIOR FILING DATE: 2003-05-03 |
| PRIOR FILING DATE:
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Best Local Similarity 100.0%; Pred. No. 2.5
Matches 21; Conservative 0; Mismatches
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        TYPE: RNA
ORGANISM: artificial
FEATURE:
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ORGANISM: artificial
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APPLICANT: Jense, martin

APPLICANT: Jense, martin

TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels

FILE REPERBENCE: UBC.P-035

CURRENT APPLICATION NUMBER: US/10/646,391A

CURRENT FILING DATE: 2003-08-21

PRIOR PLILING DATE: 2002-08-21

PRIOR PLILING DATE: 2002-12-02

PRIOR PLILING DATE: 2002-12-02

PRIOR PLILING DATE: 2002-03-03

PRIOR FILING DATE: 2002-09-03

PRIOR PLILING DATE: 2002-09-03

PRIOR PLILING DATE: 2002-09-03

PRIOR PLILING DATE: 2003-05-20

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VERSION 3.2

SOFTWARE: PATENTIN VERSION 3.2
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APPLICANT: Gleave, Martin
APPLICANT: Gleave, Martin
APPLICANT: Gleave, Martin
APPLICANT: Glanewsky, Maxim
APPLICANT: Granewsky, Maxim
APPLICANT: Granewsky, Maxim
APPLICANT: Granewsko, Ioannis
APPLICANT: Grones, Estathios
TITLE OF INVENTION: RNA! Probes Targeting Cancer-Related Proteins
FILE REFERENCE: UBC.P.03
CURRENT APPLICATION NUMBER: US/10/646,436
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/408,152
PRIOR APPLICATION NUMBER: US 60/408,152
PRIOR APPLICATION NUMBER: US 60/408,152
PRIOR PILING DATE: 2002-09-09
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 68
NUMBER OF SEQ ID NOS: 68
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Score 19; DB 17; Length 19;
Pred. No. 26;
5; Mismatches 0; Indels
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Pred. No.
                                                                                                                                                                                                                                                                                             Sequence 43, Application US/10646391A Publication No. US20040082534A1 GENERAL INFORMATION:
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1 GCAGCAGAGUCUUCAUCAU 19
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                                                                                                                                 90.5%;
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Best Local Similarity 73.7%;
Matches 14; Conservative
                                                                                                                             Query Match 90.5'
Best Local Similarity 73.7'
Matches 14; Conservative
                                TYPE: DNA
ORGANISM: HUMAN
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US-09-967-726A-4
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SEQ ID NO 4
LENGTH: 21
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APPLICANT: Signeevsky, Maxim
APPLICANT: Signeevsky, Maxim
APPLICANT: Signeevsky, Maxim
APPLICANT: Signeevsky, Maxim
APPLICANT: Beraldi, Eliana
APPLICANT: Trougakes, Ioannis
APPLICANT: Gonos, Efstathios
TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
FILE REFERENCE: UBC. P-030
CURRENT APPLICATION NUMBER: US/10/646,436
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: US 60/406,152
PRIOR APPLICATION NUMBER: US 60/408,152
PRIOR APPLICATION NUMBER: US 60/473,387
PRIOR PILING DATE: 2003-09-03
PRIOR PRIUNG DATE: 2003-09-20
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.2
SEQ ID NO 68
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                                                                              Query Match 90.5%; Score 19; DB 17; Length 19; Best Local Similarity 73.7%; Pred. No. 26; Matches 14; Conservative 5; Mismatches 0; Indels
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                                                                                                                                                                                                                                                             Sequence 68, Application US/10646436
Publication No. US20040096882A1
                                                                                                                                                1 GCAGCAGAGUCUUCAUCAU 19
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                                                                                                                                                                                                                                                                                                            APPLICANT: Jansen, Burkhard APPLICANT: Gleave, Martin
ORGANISM: artificial
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APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Miyake, Hideaki
APPLICANT: Miyake, Hideaki
APPLICANT: Miyake, Hideaki
APPLICANT: Callement Colleen
APPLICANT: Zellweger, Tobias
TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: USC. P-022
CURRENT APPLICATION NUMBER: US/09/967,726A
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
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| Sequence 4, Application US/10080794
| Publication No. US20030166591A1
| GENERAL INFORMATION:
| APPLICANT: Rennie, Paul S. |
| APPLICANT: Rennie, Paul S. |
| APPLICANT: Miyake, Hideaki |
| APPLICANT: Molay Brett P. |
| TITLE OF INVENTION: HAVING 2'-0-(2-METHOXY) ETHYL MODIFICATIONS |
| TITLE OF INVENTION: HAVING 2'-0-(2-METHOXY) ETHYL MODIFICATIONS |
| TITLE OF INVENTION: HAVING 2'-0-(2-METHOXY) ETHYL MODIFICATIONS |
| TITLE OF ILING DATE: 1090-02-22 |
| PRIOR FILING DATE: 1999-02-26 |
| PRIOR FILING DATE: 2001-08-10 |
| PRIOR FILING DATE: 2001-08-10 |
| PRIOR FILING DATE: 2001-08-10 |
| NUMBER OF SEQ ID NOS: 19 |
| SEQ ID NO 4
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                                                                                                               Length 21;
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                                                                                                               Score 19; DB 9;
Pred. No. 27;
                                                                                                                                                                       5; Mismatches
FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4
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; ENERAL INFORMATION; APPLICANT: Gleave, Martin
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Gaps

; 0

5; Mismatches

90.5%; Score 19; 73.7%; Pred. No.

DB 17; Length 21; 27; 0; Indels

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; FEATURE;
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-28
                                                                                                                                                                                                                                                                                  1 GCAGCAGAGUCUUCAUCAU 19
                                                                                                                                                                                    Query Match
Best Local Similarity 73.74
Matches 14; Conservative
SEQ ID NO 28
LENGTH: 21
TYPE: DNA
ORGANISM: artificial
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Publication No. US20040082534A1

Publication No. US20040082534A1

GENERAL INFORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Jansen, Burkhard

TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels

FILE REFERENCE: UBC.P-035

CURRENT FILING DATE: 2003-08-21

PRIOR FILING DATE: 2003-08-21

PRIOR FILING DATE: 2002-08-21

PRIOR FILING DATE: 2002-08-21

PRIOR FILING DATE: 2002-09-03

PRIOR FILING DATE: 2002-09-03

PRIOR FILING DATE: 2003-09-03

PRIOR FILING DATE: 2003-09-03

PRIOR FILING DATE: 2003-09-03

PRIOR FILING DATE: 2003-05-05-05

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn version 3.2

LENGTH: 21
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US-10-546-314A-28D.

Sequence 28, Application US/10646391A.

Publication No. US20040082534AI.

GENERAL INPORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Gleave, Martin

TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels

TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels

TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels

CURRENT APPLICATION NUMBER: US/10/646,391A

CURRENT APPLICATION NUMBER: US 60/405,193

PRIOR FILING DATE: 2002-09-21

PRIOR FILING DATE: 2002-12-02

PRIOR FILING DATE: 2002-09-03

PRIOR FILING DATE: 2003-09-03

PRIOR FILING DATE: 2003-05-20

PRIOR FILING DATE: 2003-05-20

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn version 3.2
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                                                                                             ; OTHER INFORMATION: antisense TRPM-2 ODN US-10-080-794-4
                                                                                                                                                                                                                                                                1 GCAGCAGAGUCUUCAUCAU 19
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ORGANISM: human
                           TYPE: DNA
ORGANISM: HUMAN
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-646-391A-28/c
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    LENGTH: 21
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APPLICANT: Burt, Helen
APPLICANT: Burt, Helen
APPLICANT: Springate, Christopher
APPLICANT: Springate, Christopher
APPLICANT: Gleave, Martin
TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
FILE REPERENCE: UBC.P-033
CURRENT APPLICATION NUMBER: US/10/828,394
CURRENT FILING DATE: 2004-04-19
PRIOR FILING DATE: 2003-04-18
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APPLICANT: Signaevsky, Maxim
APPLICANT: Signaevsky, Maxim
APPLICANT: Beraldi, Eliana
APPLICANT: Trougakos, Ioannis
APPLICANT: Gonos, Efstathios
TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
FILE REPERENCE: UBC. P-030
CURRENT APPLICATION NUMBER: US/10/646,436
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: US 60/405,193
PRIOR PLILNG DATE: 2002-09-03
PRIOR FILING DATE: 2002-09-03
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH: 21
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                                                                                                                                                      Sequence 9, Application US/10646436 Publication No. US20040096882A1 GENERAL INFORMATION:
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19 GCAGCAGAGTCTTCATCAT 1
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APPLICANT: Signaevsky, Maxim
APPLICANT: Signaevsky, Maxim
APPLICANT: Beraldi, Eliana
APPLICANT: Beraldi, Eliana
APPLICANT: Trougakos, Ioannis
APPLICANT: Trougakos, Ioannis
APPLICANT: Gonos, Efetathios
TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
FILE REFERENCE: UBC. 2003-08-21
CURRENT APPLICATION NUMBER: US 60/405,193
PRIOR APPLICATION NUMBER: US 60/408,152
PRIOR APPLICATION NUMBER: US 60/408,152
PRIOR APPLICATION NUMBER: US 60/473,387
PRIOR FILING DATE: 2002-09-03
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5. Application US/10828395
; Sequence 5. Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
., APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
APPLICANT: Springate, Christopher
; APPLICANT: Springate, Christopher
; APPLICANT: Springate, Christopher
; APPLICANT: Martin
; TITLE OF INVENTION MERE: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR PLING DATE: 2003-04-18
; PRIOR PLING DATE: 2003-04-18
; NUMBER OF SEC ID NOS: 23
; SOFTHARE: PatentIn version 3.2
; SEC ID NO 5.
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Pred. No. 27;
5; Mismatches 0; Indels
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                                                                                                                                                                Query Match

90.5%; Score 19; DB

Best Local Similarity 73.7%; Pred. No. 27;

Matches 14; Conservative 5; Mismatches
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Publication No. US20040096882A1
GENERAL INFORMATION:
APPLICANT: Jansen, Burkhard
APPLICANT: Gleave, Martin
APPLICANT: Signaeveky, Maxim
                                                                                                                                                                                                                                                              1 GCAGCAGAGUCUUCAUCAU 19
                                                                                                                                                                                                                                                                                            3 GCAGCAGAGTCTTCATCAT 21
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 21
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Best Local Similarity 73.7%;
Matches 14; Conservative
                                                                  TYPE: DNA
CRGANISM: human
US-10-828-394-5
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ORGANISM: human
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US-10-828-395-5
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; SEQ ID NO 66
; LONGTH: 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: human
US-10-646-436-66
Query Match
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0;
Qy 1 GCAGCAGAGUCUCAUCAU 19
Qy 1 GCAGCAGAGUCTUCATCAT 3

Search completed: May 24, 2005, 00:29:27
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